RAW SEQUENCE LISTING
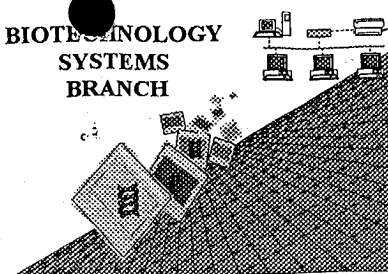# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/780,113A_

Source: _1645_

Date Processed by STIC: _5/30/2001_

RECEIVED

JUN 1 2 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   **SERIAL NUMBER:** 09/780,113A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos ·   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
Numbering   use **space characters**, instead.

4 ____ Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue n or **Xaa** represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
is Artificial Sequence

11 ____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1645

RAW SEQUENCE LISTING   DATE: 05/30/2001
PATENT APPLICATION: **US/09/780,113A**   TIME: 11:01:31

Input Set : A:\506812000120.txt
Output Set: C:\CRF3\05302001\I780113A.raw

Does Not Comply
Corrected Diskette Needed

```
 3 <110> APPLICANT: TYRRELL, JOHN V.
 4        BERGQUIST, PATRICIA R.
 5        BERGQUIST, PETER L.
 6        SCHOLIN, CHRISTOPHER A.
 8 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING RAPHIDOPHYTES
10 <130> FILE REFERENCE: 50681200121
12 <140> CURRENT APPLICATION NUMBER: 09/780,113A
13 <141> CURRENT FILING DATE: 2001-02-09
15 <150> PRIOR APPLICATION NUMBER: 09/596,136
16 60/141,362   add <150>
18 <151> PRIOR FILING DATE: 2000-06-16
19 1999-06-28   <151>
21 <160> NUMBER OF SEQ ID NOS: 30
23 <170> SOFTWARE: PatentIn Ver. 2.1
```

W--> (line 16)

W--> (line 19)

do not separate application numbers and their filing dates – group them together

e.g. <150> 60/141,362
<151> 1999-06-28

ERRORED SEQUENCES

```
259 <210> SEQ ID NO: 20
260 <211> LENGTH: 25
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificial olignucleotide
probe
267 <400> SEQUENCE: 25 20
268 tcatctttcc ctcacggtac ttgtt          25
```

oligonucleotide

E--> (line 267)
C--> (line 268)

(global error)

when using new sequence rules format, use lower-case letters for all bases (Please correct this global error)

See following page for more errors

Input Set : **A:\Pto.amc**
Output Set: **N:\CRF3\06082001\I780113A.raw**

```
295  <210> SEQ ID NO: 23
296  <211> LENGTH: 23
297  <212> TYPE: DNA
298  <213> ORGANISM: Artificial Sequence
300  <220> FEATURE:
301  <223> OTHER INFORMATION: Description of -Artificial Sequence: Artificial
303  <400> SEQUENCE: 23
```

C--> 304 agagtagctg agcacgcatc tct   *(handwritten: ← use lower-case letters)*   23

```
307  <210> SEQ ID NO: 24
308  <211> LENGTH: 687
309  <212> TYPE: DNA
310  <213> ORGANISM: Chattonella antiqua
312  <400> SEQUENCE: 24
```

```
C--> 313  ttcttgaagc ggaggaaaag aaccaactcg gattccctag taacggcgag tgaagcggga  60
     314  agagctcatg ttgtaaatct ggatgaggat tcctcgtccc gaattgtagt ctagagatgc 120
     315  gtgctcagct actctccagg gctaagtctg tttgtgaaag acagcatcat ggacggtgat 180
     316  aatccggttc ttgccttgga tgttgtagcg tcttgagccg tcctcaacga gtcgagttgc 240
     317  ttgggattgc agctctaagc gggtggtaaa ttccatctaa agctaaatat tggtgggaga 300
     318  ccgatagcga acaagtaccg tgagggaaag atgaaaagaa ctttgaaaag agagttaaat 360
     319  agtacctgaa actgctgaaa gggaagcgaa tgaagtcagt gttgctcttt gttctctgca 420
     320  tcctccctgc ggggattgtg tatcgaggac tttgagcttg tcaggatgag ttctctgccg 480
     321  cgggatatgg tttgtgagct ggatgcttct gctgaactca ctctctctgt cgtggcttgg 540
     322  actgaggttc catcttgccg ttgcctgctt gttactctcc tgttgctgtt tctgtcctac 600
     323  tgcttgcagt gttcggttgc agtgattgga ctgtgcaagt tatgcatgca aggtcaggat 660
     324  cctgacgaat ggctttatta acccgaa                                     687
```

```
327  <210> SEQ ID NO: 25
328  <211> LENGTH: 681
329  <212> TYPE: DNA
330  <213> ORGANISM: Chattonella subsalsa
332  <400> SEQUENCE: 25
```

```
C--> 333  gcggaggaaa agaaccaact cggattccct agtaacggcg agtgaagcgg gaagagctca  60
     334  tgttgtaaat ctggatgagg gttcctcgtc ccgaattgta gtctagagat gcgtgctcag 120
     335  ctactctcca gggctaagtc tgtttgtgaa agacagtgtc atggacggtg ataacccggt 180
     336  tcttgccttg gatgttgtag cgtttttgagc cgtcctcaac gagtcgagtt gcttgggatt 240
     337  gcagctctaa gtgggtggta aattccatct aaagctaaat attggtggga gaccgatagc 300
     338  gaacaagtac cgtgagggaa agatgaaaag aactttgaaa agagagttaa atagtacctg 360
     339  aaactgctga aagggaagcg aatgaagtca gtgttgctct ttgtgctctg catcctccct 420
     340  gcgggggattg tgtatcgagg actttgagct tgtcaggatg agttctctgc cgcgggatat 480
     341  gttttgtatg ctggatgctt tttgcggaac atacattctc tgtcgtggct tggactgagg 540
     342  ttccatcttg ccgttgcctg tgcgttcctc tcccgttgct gtctctgttc tactgcttgc 600
     343  agtgctcagt tgcagtagtt ggactgtgcg tattatgcat gcaaggtcag gatcctgacg 660
     344  aatggcttta ttcacccgca a                                           681
```

```
347  <210> SEQ ID NO: 26
348  <211> LENGTH: 703
349  <212> TYPE: DNA
350  <213> ORGANISM: Fibrocapsa japonica
352  <400> SEQUENCE: 26
```

```
C--> 353  cagaggaaaa gaaacaactc ggattcccta gtaacggcga gtgaagcggg aacagctcat  60
     354  gatgtaaatc tgggtgacgt ttcgttaccc cgaattgtag tctacagaag cgtgtccagc 120
```

(Handwritten margin notes: "invalid – give source of genetic material. See circled portion of Item 11 on Error Summary Sheet.")

Input Set : **A:\506812000120.txt**
Output Set: **C:\CRF3\05302001\I780113A.raw**

L:16 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:
L:19 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:
L:37 M:112 C: (48) String data converted to lower case,
L:52 M:112 C: (48) String data converted to lower case,
L:64 M:112 C: (48) String data converted to lower case,
L:76 M:112 C: (48) String data converted to lower case,
L:88 M:112 C: (48) String data converted to lower case,
L:100 M:112 C: (48) String data converted to lower case,
L:112 M:112 C: (48) String data converted to lower case,
L:124 M:112 C: (48) String data converted to lower case,
L:136 M:112 C: (48) String data converted to lower case,
L:148 M:112 C: (48) String data converted to lower case,
L:160 M:112 C: (48) String data converted to lower case,
L:172 M:112 C: (48) String data converted to lower case,
L:184 M:112 C: (48) String data converted to lower case,
L:196 M:112 C: (48) String data converted to lower case,
L:208 M:112 C: (48) String data converted to lower case,
L:220 M:112 C: (48) String data converted to lower case,
L:232 M:112 C: (48) String data converted to lower case,
L:244 M:112 C: (48) String data converted to lower case,
L:256 M:112 C: (48) String data converted to lower case,
L:267 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:25
L:268 M:112 C: (48) String data converted to lower case,
L:280 M:112 C: (48) String data converted to lower case,
L:292 M:112 C: (48) String data converted to lower case,
L:304 M:112 C: (48) String data converted to lower case,
L:313 M:112 C: (48) String data converted to lower case,
L:314 M:112 C: (48) String data converted to lower case,
L:315 M:112 C: (48) String data converted to lower case,
L:316 M:112 C: (48) String data converted to lower case,
L:317 M:112 C: (48) String data converted to lower case,
L:318 M:112 C: (48) String data converted to lower case,
L:319 M:112 C: (48) String data converted to lower case,
L:320 M:112 C: (48) String data converted to lower case,
L:321 M:112 C: (48) String data converted to lower case,
L:322 M:112 C: (48) String data converted to lower case,
L:323 M:112 C: (48) String data converted to lower case,
L:324 M:112 C: (48) String data converted to lower case,
L:333 M:112 C: (48) String data converted to lower case,
L:334 M:112 C: (48) String data converted to lower case,
L:335 M:112 C: (48) String data converted to lower case,
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L:337 M:112 C: (48) String data converted to lower case,
L:338 M:112 C: (48) String data converted to lower case,
L:339 M:112 C: (48) String data converted to lower case,
L:340 M:112 C: (48) String data converted to lower case,
L:341 M:112 C: (48) String data converted to lower case,
L:342 M:112 C: (48) String data converted to lower case,

```
L:343 M:112 C: (48) String data converted to lower case,
L:344 M:112 C: (48) String data converted to lower case,
L:353 M:112 C: (48) String data converted to lower case,
L:354 M:112 C: (48) String data converted to lower case,
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L:402 M:112 C: (48) String data converted to lower case,
L:403 M:112 C: (48) String data converted to lower case,
L:404 M:112 C: (48) String data converted to lower case,
L:418 M:112 C: (48) String data converted to lower case,
L:430 M:112 C: (48) String data converted to lower case,
```